

SEQUENCE LISTING

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OCT 12 2001
TECH CENTER 1600/2900

(1) GENERAL INFORMATION:

- (i) APPLICANT: Pastan, Ira
Chang, Kai
- (ii) TITLE OF INVENTION: Mesothelin, a Differentiation Antigen
Present on Mesothelium, Mesotheliomas and Ovarian Cancers
and Methods and Kits for Targeting the Antigen
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Townsend and Townsend and Crew LLP
(B) STREET: Two Embarcadero Center, Eighth Floor
(C) CITY: San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Not yet assigned
(B) FILING DATE: Not yet assigned
(C) CLASSIFICATION:
- B 34* (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/776,271
(B) FILING DATE: 01-DEC-1998
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: WO PCT/US97/00224
(B) FILING DATE: 03-JAN-1997
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/010,166
(B) FILING DATE: 05-JAN-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Faris, Susan K.
(B) REGISTRATION NUMBER: 41,739
(C) REFERENCE/DOCKET NUMBER: 015280-259110US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (415) 576-0200
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 100..1986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:


AGGAATTCCG GTGGCCGGCC ACTCCCGTCT GCTGTGACGC GCGGACAGAG AGCTACCGGT 60

GGACCCACGG TGCCTCCCTC CCTGGGATCT ACACAGACC ATG GCC TTG CAA CGG 114
Met Ala Leu Gln Arg
1 5

CTC GAC CCC TGT TGG TCC TGT GGG GAC CGC CCT GGC AGC CTC CTG TTC 162
Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro Gly Ser Leu Leu Phe
10 15 20

CTG CTC TTC AGC CTC GGA TGG GTG CAT CCC GCG AGG ACC CTG GCT GGA 210
Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala Arg Thr Leu Ala Gly
25 30 35

GAG ACA GGG ACG GAG TCT GCC CCC CTG GGG GGA GTC CTG ACA ACC CCC 258
Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly Val Leu Thr Thr Pro
40 45 50

 CAT AAC ATT TCC AGC CTC TCC CCT CGC CAA CTC CTT GGC TTC CCG TGT 306
His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu Leu Gly Phe Pro Cys
55 60 65

GCG GAG GTG TCC GGC CTG AGC ACG GAG CGT GTC CGG GAG CTG GCT GTG 354
Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val Arg Glu Leu Ala Val
70 75 80 85

GCC TTG GCA CAG AAG AAT GTC AAG CTC TCA ACA GAG CAG CTG CGC TGT 402
Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr Glu Gln Leu Arg Cys
90 95 100

CTG GCT CAC CGG CTC TCT GAG CCC CCC GAG GAC CTG GAC GCC CTC CCA 450
Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp Leu Asp Ala Leu Pro
105 110 115

TTG GAC CTG CTG CTA TTC CTC AAC CCA GAT GCG TTC TCG GGG CCC CAG 498
Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala Phe Ser Gly Pro Gln
120 125 130

GCC TGC ACC CGT TTC TTC TCC CGC ATC ACG AAG GCC AAT GTG GAC CTG 546
Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys Ala Asn Val Asp Leu
135 140 145

CTC	CCG	AGG	GGG	GCT	CCC	GAG	CGA	CAG	CGG	CTG	CTG	CCT	GCG	GCT	CTG	594
Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln	Arg	Leu	Leu	Pro	Ala	Ala	Leu	
150					155					160					165	
GCC	TGC	TGG	GGT	GTG	CGG	GGG	TCT	CTG	CTG	AGC	GAG	GCT	GAT	GTG	CGG	642
Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu	Leu	Ser	Glu	Ala	Asp	Val	Arg	
			170						175					180		
GCT	CTG	GGA	GGC	CTG	GCT	TGC	GAC	CTG	CCT	GGG	CGC	TTT	GTG	GCC	GAG	690
Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu	Pro	Gly	Arg	Phe	Val	Ala	Glu	
			185					190					195			
TCG	GCC	GAA	GTG	CTG	CTA	CCC	CGG	CTG	GTG	AGC	TGC	CCG	GGA	CCC	CTG	738
Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu	Val	Ser	Cys	Pro	Gly	Pro	Leu	
		200					205					210				
GAC	CAG	GAC	CAG	CAG	GAG	GCA	GCC	AGG	GCG	GCT	CTG	CAG	GGC	GGG	GGA	786
Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg	Ala	Ala	Leu	Gln	Gly	Gly	Gly	
	215					220					225					
CCC	CCC	TAC	GGC	CCC	CCG	TCG	ACA	TGG	TCT	GTC	TCC	ACG	ATG	GAC	GCT	834
Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp	Ser	Val	Ser	Thr	Met	Asp	Ala	
230					235					240					245	
CTG	CGG	GGC	CTG	CTG	CCC	GTG	CTG	GGC	CAG	CCC	ATC	ATC	CGC	AGC	ATC	882
Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly	Gln	Pro	Ile	Ile	Arg	Ser	Ile	
			250					255						260		
CCG	CAG	GGC	ATC	GTG	GCC	GCG	TGG	CGG	CAA	CGC	TCC	TCT	CGG	GAC	CCA	930
Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg	Gln	Arg	Ser	Ser	Arg	Asp	Pro	
			265					270					275			
TCC	TGG	CGG	CAG	CCT	GAA	CGG	ACC	ATC	CTC	CGG	CCG	CGG	TTC	CGG	CGG	978
Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile	Leu	Arg	Pro	Arg	Phe	Arg	Arg	
		280					285					290				
GAA	GTG	GAG	AAG	ACA	GCC	TGT	CCT	TCA	GGC	AAG	AAG	GCC	CGC	GAG	ATA	1026
Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser	Gly	Lys	Lys	Ala	Arg	Glu	Ile	
	295					300					305					
GAC	GAG	AGC	CTC	ATC	TTC	TAC	AAG	AAG	TGG	GAG	CTG	GAA	GCC	TGC	GTG	1074
Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys	Trp	Glu	Leu	Glu	Ala	Cys	Val	
310					315					320					325	
GAT	GCG	GCC	CTG	CTG	GCC	ACC	CAG	ATG	GAC	CGC	GTG	AAC	GCC	ATC	CCC	1122
Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met	Asp	Arg	Val	Asn	Ala	Ile	Pro	
			330						335					340		
TTC	ACC	TAC	GAG	CAG	CTG	GAC	GTC	CTA	AAG	CAT	AAA	CTG	GAT	GAG	CTC	1170
Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu	Lys	His	Lys	Leu	Asp	Glu	Leu	
			345				350						355			
TAC	CCA	CAA	GGT	TAC	CCC	GAG	TCT	GTG	ATC	CAG	CAC	CTG	GGC	TAC	CTC	1218
Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val	Ile	Gln	His	Leu	Gly	Tyr	Leu	
		360					365					370				
TTC	CTC	AAG	ATG	AGC	CCT	GAG	GAC	ATT	CGC	AAG	TGG	AAT	GTG	ACG	TCC	1266
Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile	Arg	Lys	Trp	Asn	Val	Thr	Ser	
	375					380					385					

B4
SW

CTG GAG ACC CTG AAG GCT TTG CTT GAA GTC GAC AAA GGG CAC GAA ATG	1314
Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp Lys Gly His Glu Met	
390 395 400 405	
AGT CCT CAG GCT CCT CGG CGG CCC CTC CCA CAG GTG GCC ACC CTG ATC	1362
Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln Val Ala Thr Leu Ile	
410 415 420	
GAC CGC TTT GTG AAG GGA AGG GGC CAG CTA GAC AAA GAC ACC CTA GAC	1410
Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp Lys Asp Thr Leu Asp	
425 430 435	
ACC CTG ACC GCC TTC TAC CCT GGG TAC CTG TGC TCC CTC AGC CCC GAG	1458
Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys Ser Leu Ser Pro Glu	
440 445 450	
GAG CTG AGC TCC GTG CCC CCC AGC AGC ATC TGG GCG GTC AGG CCC CAG	1506
Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp Ala Val Arg Pro Gln	
455 460 465	
GAC CTG GAC ACG TGT GAC CCA AGG CAG CTG GAC GTC CTC TAT CCC AAG	1554
Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp Val Leu Tyr Pro Lys	
470 475 480 485	
GCC CGC CTT GCT TTC CAG AAC ATG AAC GGG TCC GAA TAC TTC GTG AAG	1602
Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser Glu Tyr Phe Val Lys	
490 495 500	
ATC CAG TCC TTC CTG GGT GGG GCC CCC ACG GAG GAT TTG AAG GCG CTC	1650
Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu	
505 510 515	
AGT CAG CAG AAT GTG AGC ATG GAC TTG GCC ACG TTC ATG AAG CTG CGG	1698
Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg	
520 525 530	
ACG GAT GCG GTG CTG CCG TTG ACT GTG GCT GAG GTG CAG AAA CTT CTG	1746
Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu	
535 540 545	
GGA CCC CAC GTG GAG GGC CTG AAG GCG GAG GAG CCG CAC CGC CCG GTG	1794
Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val	
550 555 560 565	
CGG GAC TGG ATC CTA CGG CAG CGG CAG GAC GAC CTG GAC ACG CTG GGG	1842
Arg Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly	
570 575 580	
CTG GGG CTA CAG GGC GGC ATC CCC AAC GGC TAC CTG GTC CTA GAC CTC	1890
Leu Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu	
585 590 595	
AGC GTG CAA GAG ACC CTC TCG GGG ACG CCC TGC CTC CTA GGA CCT GGA	1938
Ser Val Gln Glu Thr Leu Ser Gly Thr Pro Cys Leu Leu Gly Pro Gly	
600 605 610	
CCT GTT CTC ACC GTC CTG GCA CTG CTC CTA GCC TCC ACC CTG GCC	1983
Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala	
615 620 625	
TGAGGGCCCC ACTCCCTTGC TGGCCCCAGC CCTGCTGGGG ATCCCCGCCT GGCCAGGAGC	2043

BA

AGGCACGGGT GATCCCCGTT CCACCCCAAG AGAACTCGCG CTCAGTAAAC GGGAACATGC 2103
 CCCCTGCAGA CAAAAAAAAA AAAAAAAAAA AAAAA 2138

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Leu Gln Arg Leu Asp Pro Cys Trp Ser Cys Gly Asp Arg Pro
 1 5 10 15
 Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val His Pro Ala
 20 25 30
 Arg Thr Leu Ala Gly Glu Thr Gly Thr Glu Ser Ala Pro Leu Gly Gly
 35 40 45
 Val Leu Thr Thr Pro His Asn Ile Ser Ser Leu Ser Pro Arg Gln Leu
 50 55 60
 Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu Arg Val
 65 70 75 80
 Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu Ser Thr
 85 90 95
 Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro Glu Asp
 100 105 110
 Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro Asp Ala
 115 120 125
 Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile Thr Lys
 130 135 140
 Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln Arg Leu
 145 150 155 160
 Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu Leu Ser
 165 170 175
 Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu Pro Gly
 180 185 190
 Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu Val Ser
 195 200 205
 Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg Ala Ala
 210 215 220
 Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp Ser Val
 225 230 235 240

Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly Gln Pro
 245 250 255
 Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg Gln Arg
 260 265 270
 Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile Leu Arg
 275 280 285
 Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser Gly Lys
 290 295 300
 Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys Trp Glu
 305 310 315 320
 Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met Asp Arg
 325 330 335
 Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu Lys His
 340 345 350
 Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val Ile Gln
 355 360 365
 His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile Arg Lys
 370 375 380
 Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu Val Asp
 385 390 395 400
 Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu Pro Gln
 405 410 415
 Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln Leu Asp
 420 425 430
 Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr Leu Cys
 435 440 445
 Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser Ile Trp
 450 455 460
 Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln Leu Asp
 465 470 475 480
 Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn Gly Ser
 485 490 495
 Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu
 500 505 510
 Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu Ala Thr
 515 520 525
 Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val Ala Glu
 530 535 540
 Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala Glu Glu
 545 550 555 560

B7
 nf

Arg	His	Arg	Pro	Val	Arg	Asp	Trp	Ile	Leu	Arg	Gln	Arg	Gln	Asp	Asp	
				565					570					575		
Leu	Asp	Thr	Leu	Gly	Leu	Gly	Leu	Gln	Gly	Gly	Ile	Pro	Asn	Gly	Tyr	
				580					585					590		
Leu	Val	Leu	Asp	Leu	Ser	Val	Gln	Glu	Thr	Leu	Ser	Gly	Thr	Pro	Cys	
				595					600					605		
Leu	Leu	Gly	Pro	Gly	Pro	Val	Leu	Thr	Val	Leu	Ala	Leu	Leu	Leu	Ala	
				610					615					620		
Ser	Thr	Leu	Ala													
625																

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly Gly Gly Gly Ser
1 5

B² (2)

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Glu Asp Leu Lys
1 5

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Glu Asp Leu
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

BZ ✓ (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Asp Glu Leu
1

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Arg Pro Arg Phe Arg Arg
1 5
